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### General information about the entry

Entry name	Q9Y272
Primary accession number	Q9Y272
Secondary accession numbers	None
Entered in TrEMBL in	Release 12, November 1999
Sequence was last modified in	Release 12, November 1999
Annotations were last modified in	Release 23, February 2003

### Name and origin of the protein

Protein name	RAS-related protein
Synonyms	Activator of G-protein signaling RAS, dexamethasone-induced 1
Gene name	AGS1 or DEXRAS1 or RASD1
From	<u>Homo sapiens (Human)</u> [TaxID: 9606]
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Mammalia</u> ; <u>Eutheria</u> ; <u>Primates</u> ; <u>Catarrhini</u> ; <u>Hominidae</u> ; <u>Homo</u> .

### References

## [1] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Pituitary;Kemppainen R.J.;

"Identification of human pituitary Dexras1.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

## [2] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Liver;Cismowski M.J., Takesono A., Ma C., Lizano J.S., Xie X., Fuernkranz H., Lanier S.M., Duzic E.;"Functional genomics in the yeast *Saccharomyces cerevisiae*: cloning of mammalian G-protein activators.";

Nat. Biotechnol. 0:0-0(1999).

## [3] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=20135605; PubMed=10673050; [NCBI, ExPASy, EBI, Israel, Japan]Tu Y., Wu C.;

"Cloning, expression and characterization of a novel human Ras-related protein that is regulated by glucocorticoid hormone.";

Biochim. Biophys. Acta 1489:452-456(1999).

## [4] SEQUENCE FROM NUCLEIC ACID.

Cismowski M.J., Xie X., Duzic E.;

"Genomic sequence of the human ras-related G-protein activator AGS1.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

## [5] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Brain;Strausberg R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

## [6] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Brain;Puhl H.L., Ikeda S.R., Aronstam R.S.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

**Comments**

None

**Cross-references**

EMBL	AF153192; AAD34621.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
	AF069506; AAD34206.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
	AF172846; AAF01364.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
	AF222979; AAG44256.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
	BC018041; AAH18041.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
	AF498923; AAM21071.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
HSSP	P10114; 1KAO. [ <a href="#">HSSP ENTRY</a> / <a href="#">PDB</a> ]
Ensembl	Q9Y272; Homo sapiens. [ <a href="#">Entry</a> / <a href="#">Contig view</a> ]
InterPro	IPR001806; Ras_trnsfrmng.
	IPR005225; Small_GTP.
	<a href="#">Graphical view of domain structure.</a>
Pfam	PF00071; ras; 1.
PRINTS	PR00449; RASTRNSFRMNG.
TIGRFAMs	TIGR00231; small_GTP; 1.
ProDom	[ <a href="#">Domain structure</a> / <a href="#">List of seq. sharing at least 1 domain</a> ].
ProtoMap	Q9Y272.
PRESAGE	Q9Y272.
ModBase	Q9Y272.
SWISS-2DPAGE	<a href="#">Get region on 2D PAGE.</a>

**Keywords**GTP-binding.**Features**

None

**Sequence information**Length: **281 AA** Molecular weight: **31642 Da** CRC64: **06C3C4417E4A69BD** [This is a checksum on the sequence]

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      10      20      30      40      50      60
      |      |      |      |      |      |
MKLAAMIKKM CPSDSELSIP AKNCYRMVIL GSSKVGKTAI VSRFLTGRFE DAYTPTIEDF
      70      80      90     100     110     120
      |      |      |      |      |      |
HRKFYSIRGE VYQLDILDTS GNHPFPAMRR LSILTGDVFI LVFSLDNRDS FEEVQRLRQQ
     130     140     150     160     170     180
      |      |      |      |      |      |
ILDTSKCLKN KTKENVDPVL VICGNKGDRD FYREVDQREI EQLVGDDPQR CAYFEISAKK
     190     200     210     220     230     240
      |      |      |      |      |      |
NSSLDQMFRF LFAMAKLPSE MSPDLHRKVS VQYCDVLHKK ALRNKLLRA GSGGGGGDPG
     250     260     270     280
      |      |      |      |
DAFGIVAPFA RRPSVHSDLM YIREKASAGS QAKDKERCVI S

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